

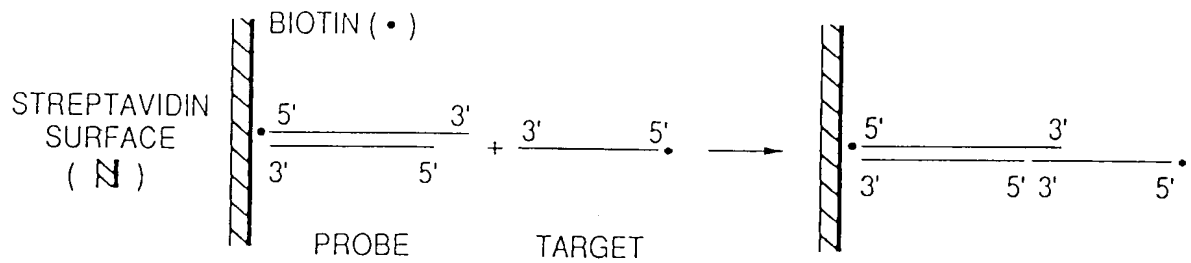


FIG. 1

NUCLEIC ACID STRUCTURE	CALCULATED $T_m$ ( $^{\circ}\text{C}$ , AVERAGE BASE COMPOSITION)					
	n = 8	7	6	5		
	38	33	25	15		
	33	25	15	3		
	25	15	3	-14		
	51	46	40	31		
	46	40	31	21		
	40	41	21	11		

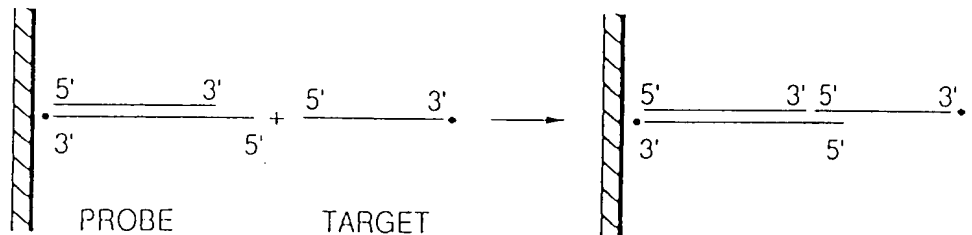


FIG. 2A



BASIC SCHEME FOR POSITIONAL SBH

FIG. 2B



ALTERNATE SCHEME



FIG. 3A

LIGATION OF TARGET DNA WITH PROBE

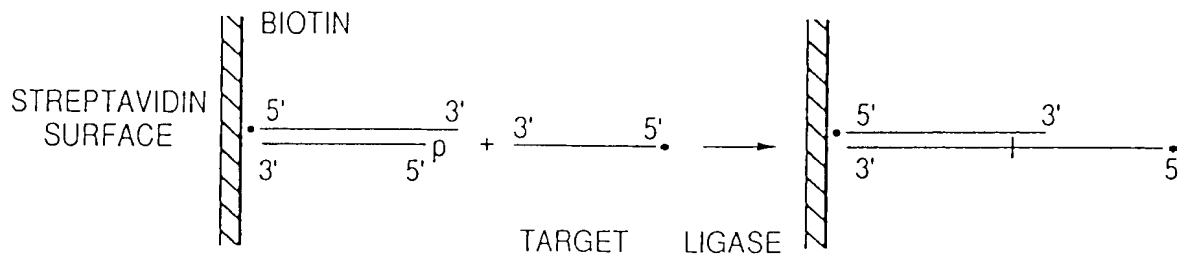


FIG. 3B

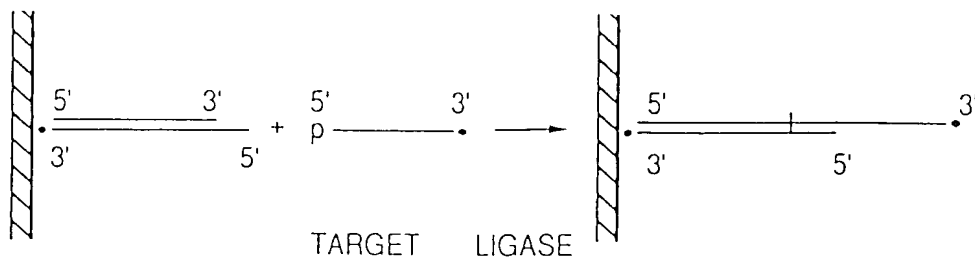




FIG. 4

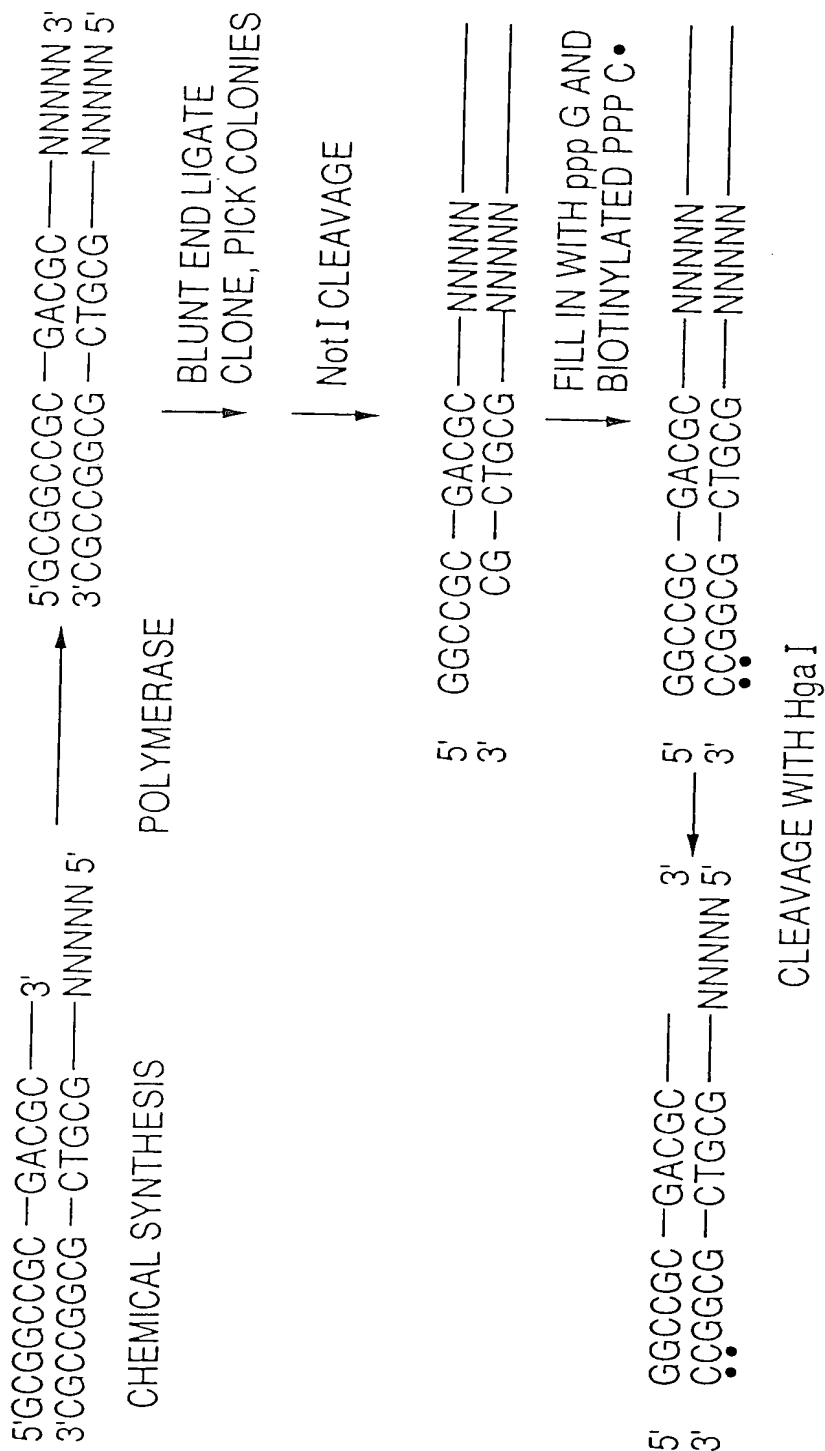
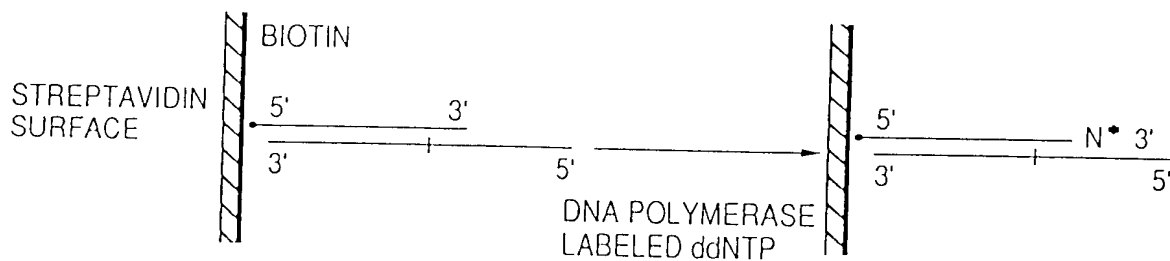


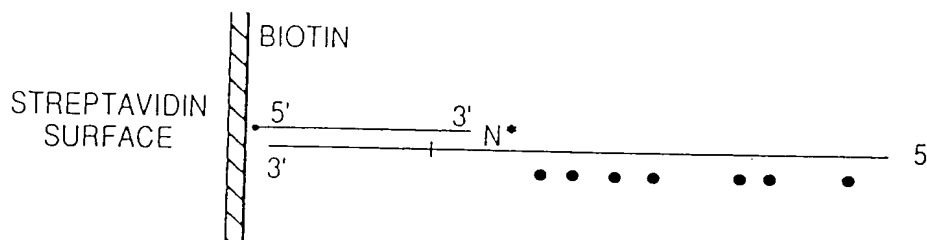


FIG. 5



READING AN EXTRA TARGET BASE BY 3' EXTENSION OF THE PROBE

FIG. 7



POSITIONAL INFORMATION FROM RATIO OF INTERNAL LABEL (•) TO  
EXTENSION LABEL (\*). A 5' LABEL COULD ALSO BE USED.

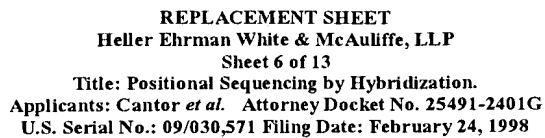
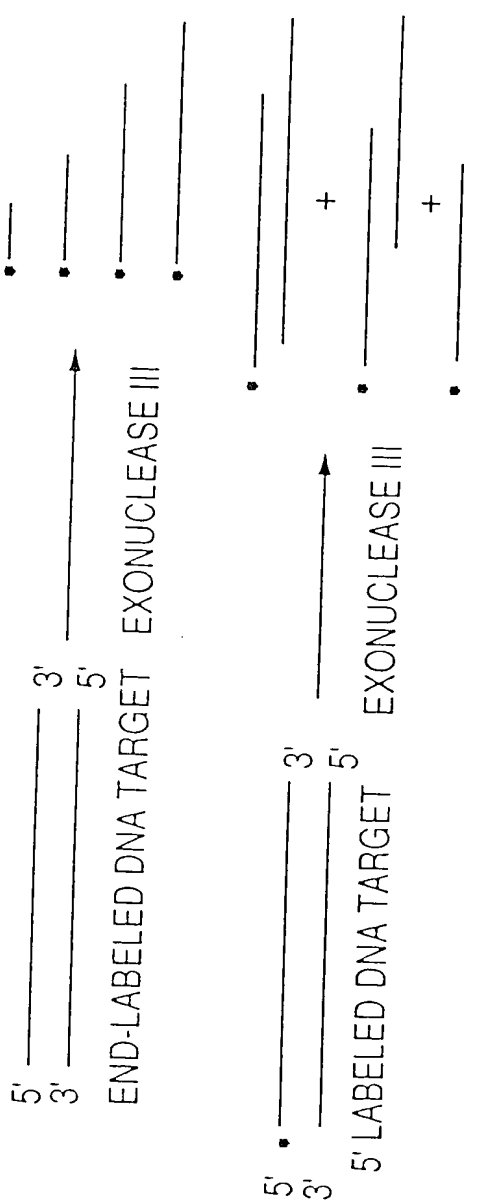


FIG. 6

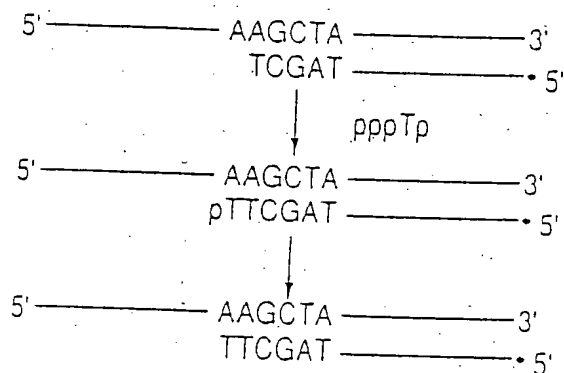


# PREPARATION OF A NESTED SET OF DNAs



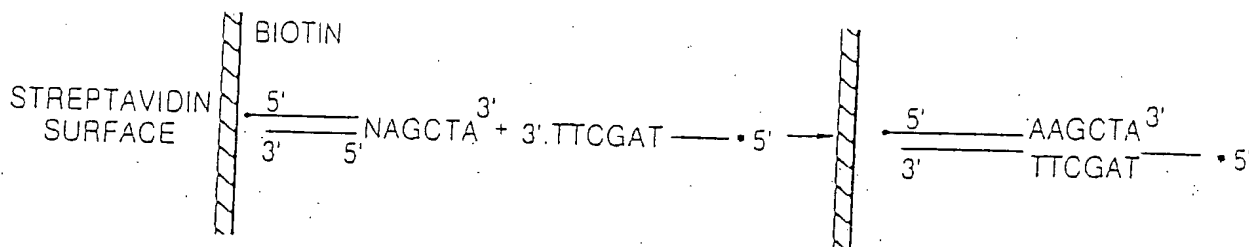
FIG. 8

READING AN EXTRA TARGET BASE



EXTENSION WILL FAIL WITH pppAp, pppGp, AND pppCp

A. 3' EXTENSION OF THE TARGET WITH A pppNp PRIOR TO  
PHOSPHATASE TREATMENT



ARRAY WITH ONE DEGENERATE BASE

B. HYBRIDIZATION AND LIGATION



## FIG. 9

CHAIN TERMINATOR:	LABEL INTENSITY		
	T	G	A
SEQUENCE			
GGAAT	2A, 2G	—	2G
AAGGT	2A, 2G	2A	—
GAAGT	2A, 2G	—	1G
AGGAT	2A, 2G	1A	—
AGAGT	2A, 2G	1A	—
GAGAT	2A, 2G	—	1G
GGGAT	1A, 3G	—	3G
GGAGT	1A, 3G	—	2G
GAGGT	1A, 3G	—	1G
AGGGT	1A, 3G	1A	—
AAAGT	3A, 1G	3A	—
AAGAT	3A, 1G	2A	—
AGAAT	3A, 1G	1A	—
GAAAT	3A, 1G	—	1G
GGGGT	4G	—	1T, 4G*
AAAAT	4A	1T, 4*	—

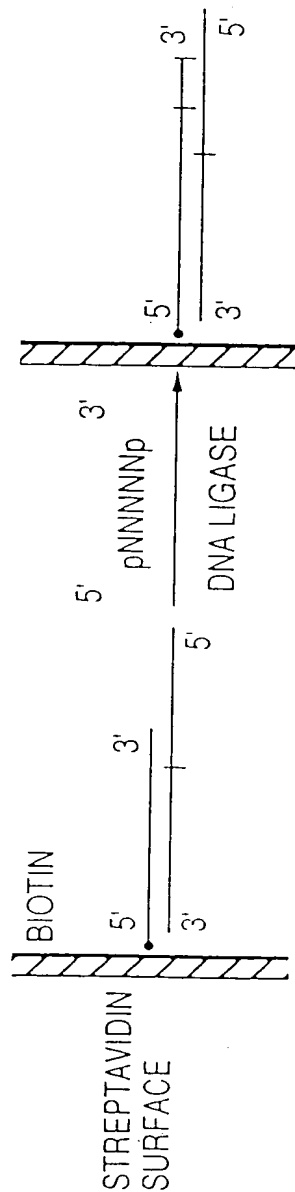
FOUR COLOR ANALYSIS OF SEQUENCE EXTENSION OF THE 3' END OF THE PROBE. LABEL INTENSITY SHOWN DOES NOT INCLUDE CONTRIBUTION FROM THE 3' TERMINATOR.

\* PLUS ADDITIONAL POSSIBLE RESIDUES





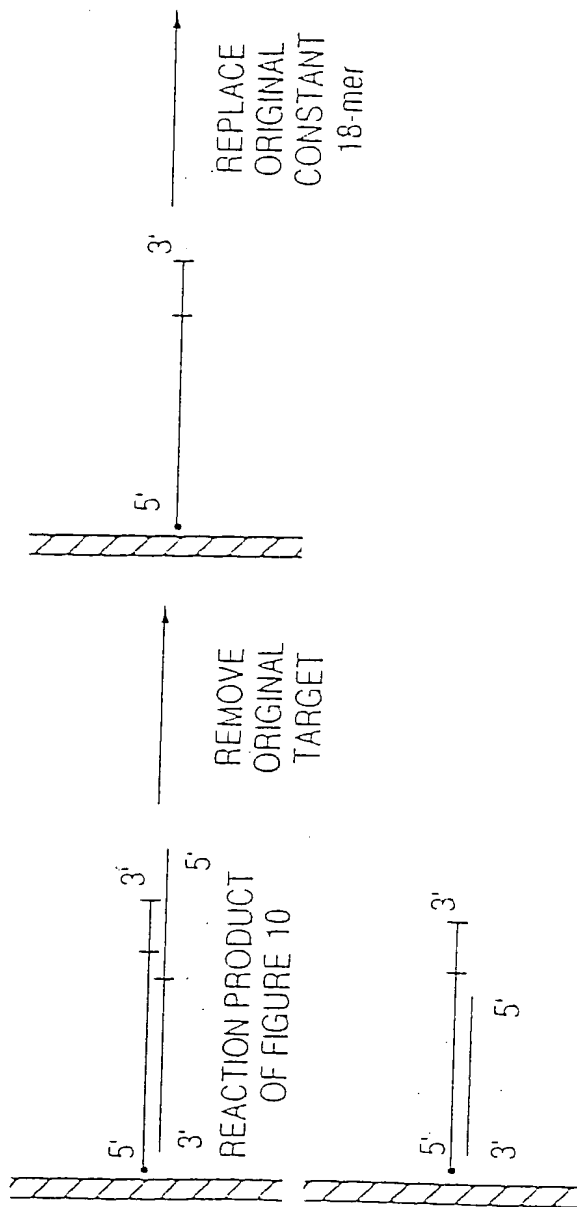
FIG. 10



EXTENSION OF THE PROBE BY LIGATION OF A BLOCKED PENTANUCLEOTIDE.  
THE PENTANUCLEOTIDE IS 3'-BLOCKED TO PREVENT POLYMERIZATION.



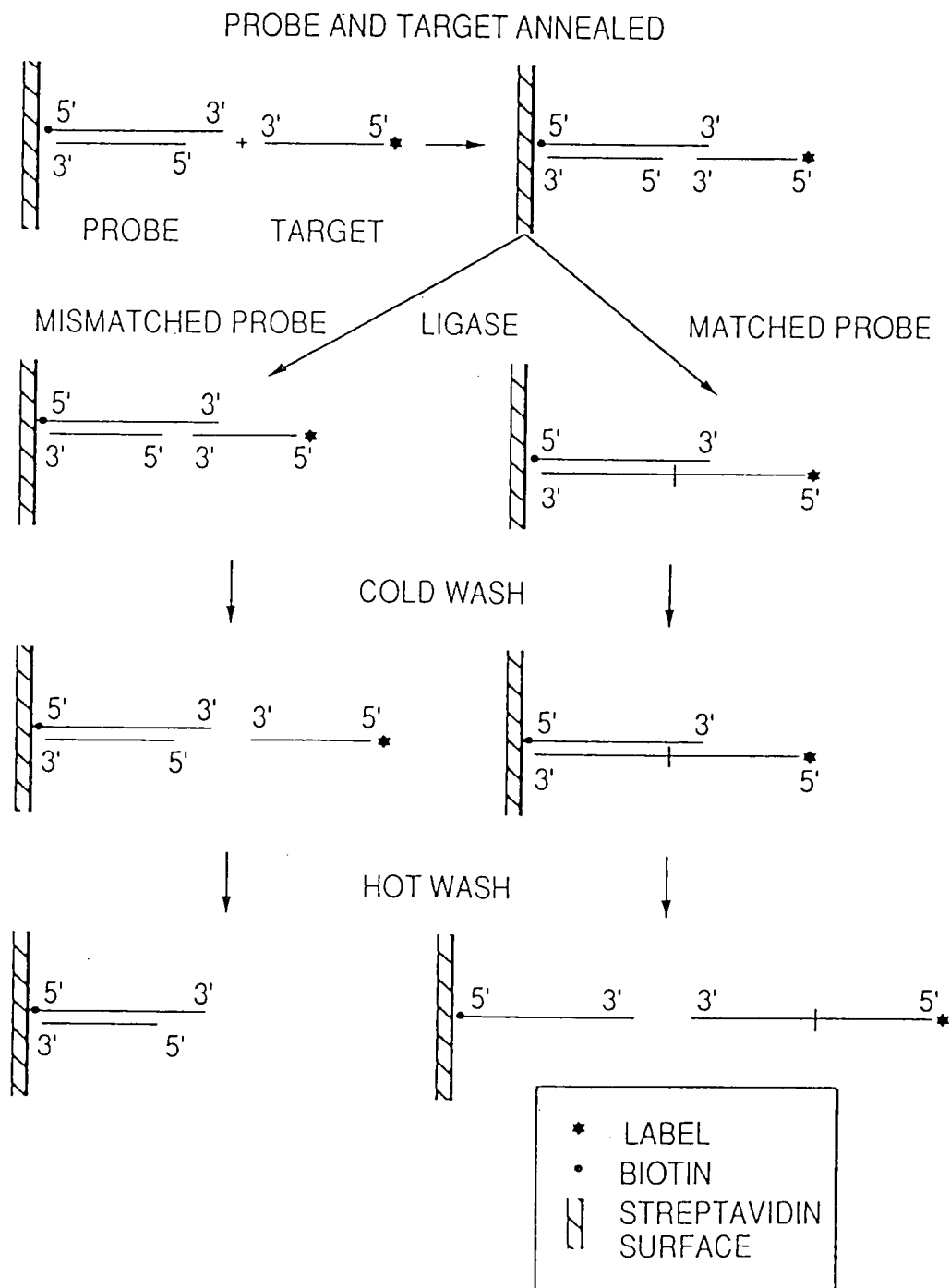
FIG. 11



PREPARATION OF A CUSTOMIZED PROBE CONTAINING A 10 bp SEQUENCE  
PRESENT IN THE ORIGINAL TARGET DNA



FIG. 12



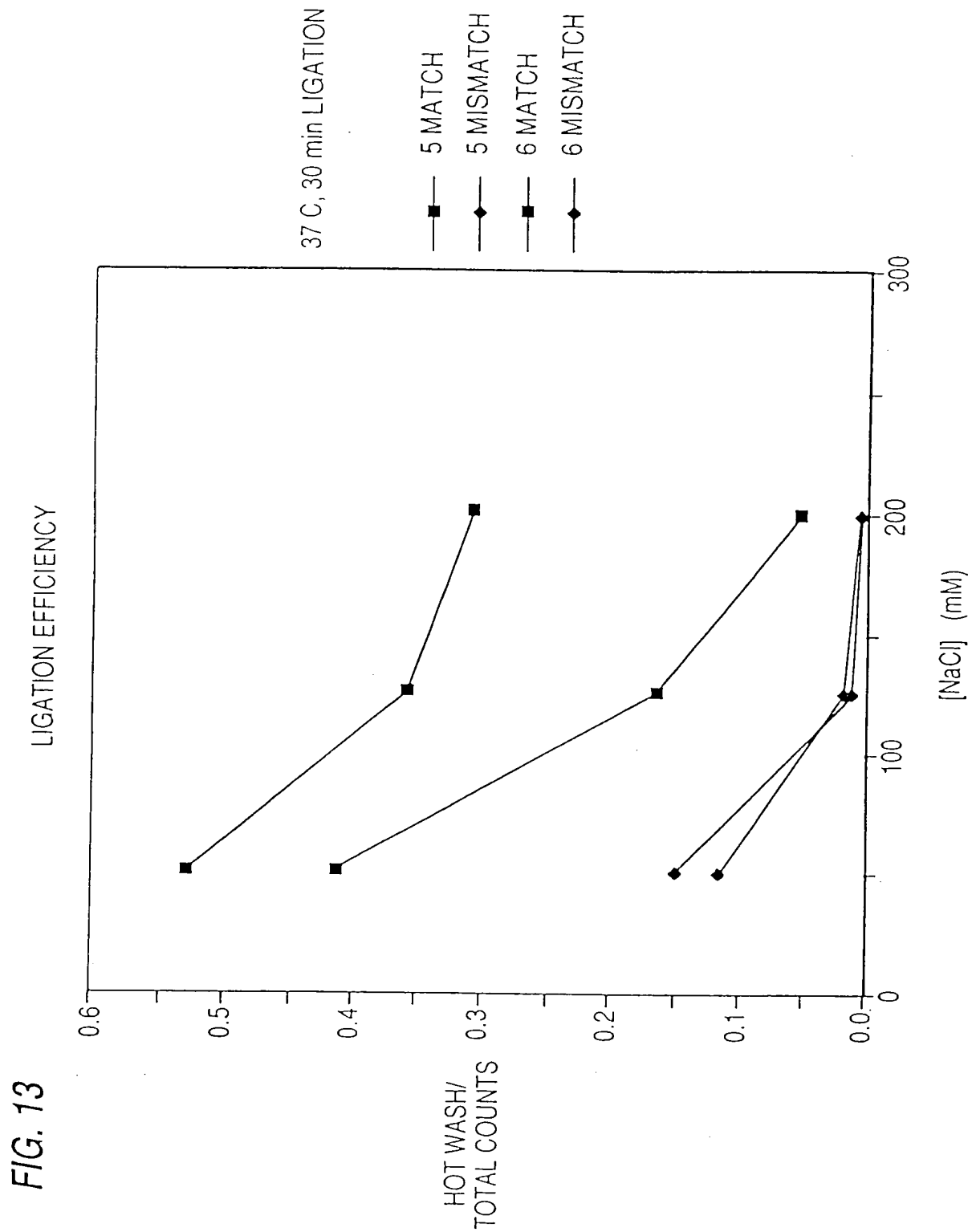




FIG. 14

